

#2



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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/087,137

DATE: 03/19/2002

TIME: 16:00:18

Input Set : A:\EP.txt

Output Set: N:\CRF3\03192002\J087137.raw

3 <110> APPLICANT: Dedera, Douglas
 4 Yamazaki, Victoria
 5 Asundi, Vinod
 6 Liu, Chenghua
 7 Tang, Y. Tom
 8 Drmanac, Radoje T.
 10 <120> TITLE OF INVENTION: Methods of Therapy and Diagnosis Using Insulin-like Growth Factor Binding
 11 Protein-like Polypeptides and Polynucleotides
 13 <130> FILE REFERENCE: HYS-38CIP
 C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/087,137
 16 <141> CURRENT FILING DATE: 2002-02-27
 18 <150> PRIOR APPLICATION NUMBER: 09/784,748
 19 <151> PRIOR FILING DATE: 2001-02-14
 21 <150> PRIOR APPLICATION NUMBER: 09/649,167
 22 <151> PRIOR FILING DATE: 2000-08-23
 24 <150> PRIOR APPLICATION NUMBER: 09/540,217
 25 <151> PRIOR FILING DATE: 2000-03-31
 27 <160> NUMBER OF SEQ ID NOS: 14
 29 <170> SOFTWARE: PatentIn version 3.1
 31 <210> SEQ ID NO: 1
 32 <211> LENGTH: 375
 33 <212> TYPE: DNA
 34 <213> ORGANISM: Homo sapiens
 36 <400> SEQUENCE: 1
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 39 gcgacggccc ttgcgagttc gtcctgtgg tgcgttgtcc tccccgaagt gttcacaaacg 120
 41 tcaccggggc gcaggtgggc ctgtcctgtg aagtggggc tgcgcctacc ccagtcatca 180
 43 cgtggagaaa ggtcacgaag tcccctgagg gcacccaagc actggaggag ctgcctgggg 240
 45 accatgtcaa tatagctgtc caagtgcgag ggggccttc tgaccatgag gccacggcct 300
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 49 acatggtggg agagg 375
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 53 <211> LENGTH: 473
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 55 <213> ORGANISM: Homo sapiens
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 60 gtaaaatacag gagcttcac tttccagctc ccgtatgaccg catgtgtatgg agaaaatgtac 120
 62 atgttctaag tcattttcag tattttacac ccatgttacg agatatttga ggtggcttat 180
 64 aagacctgtta gaaaaaaagaa gaaaaatacgt taaatggagg aaaccaggaa aagagcaaaa 240
 66 gaagagtagg gacatactta gatgagcagt agaatccctg gtatattctg cacacatctc 300
 68 cctctgagct tcttagcatg caaagacaag agctgtgaac atgaagggtgt gtccatgaga 360
 70 tgaaaagacc agttgtgttt tggggctgga gggatatattt cctctgtatt ctttttagaaa 420

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83	gcgcacggccc ttgcgagttc gctcctgtgg tcgtcggtcc tccccgaatg gttcacaaacg	120
85	tcaccggggc gcagggtggc ctgtcctgtg aagtggggc tggccttacc ccagtcatca	180
87	cgtggagaaa ggtcacgaag tccctgagg gcacccaagc actggaggag ctgcctgggg	240
89	accatgtcaa tatagtgtc caagtgcgag gggcccttc tgaccatgag gccacggcct	300
91	gtattttgtat caacccttg cgaaaggagg atgagggtgt gtaccagtgc catgcagcca	360
93	acatgggtggg agagg	375
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104	ctgtcccgga gcaagccatg cccgcgttgt ctctgctctt gccgcgtctg cttctgtgc	120
106	tgcgtccgtcgt gctgccgcgc ctgtcccgaa gccttggat cccgcacgtg ggcggcggc	180
108	gcucccaatgt tggtccgtgc cggccagagg gctgcccggc gcctgcgcgc tgccggcgc	240
110	ccgggatctc ggcgtctgac gatgtcggtc gctgcgcgc ctgcctggaa gccgagggcg	300
112	cgagctgcgg gggccgcgcg ggcggggcgt gtggcccccgt ctggatgtc gcgagccagg	360
114	ccgcgtgggc acgcggcggag ggcacccggc tctgcgtgt cccgcacgcgc ggcacccgtct	420
116	ggggcgtccga cggtcgtcgt taccccgacg tctgcgcgtc ggcgcgtgc gtcggcaca	480
118	cgcggccgcgc gcaccccggt cacctgcaca aggccgcgcga cggcccttgc gagttcggtc	540
120	ctatcaactcgt ttttataac tgctttccctc agccgttaat tacacaggcaa ttcttttgt	600
122	ctccagacag gagacagagt gagaccctgt ctaaaaaagaa gaagaagaag gaggaggagg	660
124	aggaggagga ggaggagggg gaggaggaga aggaagaaga aggtatgc当地 agcaatttcc	720
126	aacacacccat taactttaaa gaaatctcag agggatggaa agatgttt tcattccagc	780
128	catcaatgtat cgatataatt gacgaggcgt ctacactgca ctggcccaa cacgtgtgg	840
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132	cccgaaatgt tcacaacgtc accggggcgc aggtggcctt gtcgtgtgaa gtgagggtcg	960
134	tgccttacccc agtcatcactcgtggagaaagg tcacaaatgtcgtcc acggatgtggc acccaagcac	1020
136	tggaggaggt gcctggggac catgtcaata tagctgtccaa agtgcgagggg ggccttctg	1080
138	accatgtggc cacggcctgg atttgggtgt cagacctgca tcattgtctg aaggctctcc	1140
140	ccacccatc ctactccacg accctttctc ttccacagggt gtttctcttatacatctct	1200
142	tgcacatgg acccttacgtt ggtgcgtcgtca ttggaggc cccacccttag	1250
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159	gctgtccgg	agcaagcc	atg	ccg	cgc	ttg	tct	ctg	ctc	ttg	ccg	ctg	ctg	111
160			Met	Pro	Arg	Leu	Ser	Leu	Leu	Leu	Pro	Leu	Leu	
161			1			5					10			
163	ctt	ctg	ctg	ctg	ccg	ctg	ctg	ccg	ccg	ctg	tcc	ccg	agc	159
164	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Pro	Pro	Leu	Ser	Pro	Ser	Gly
165			15			20					25			
167	atc	cgc	gac	gtg	ggc	ggc	cg	cgc	ccc	aag	tgt	ggt	ccg	207
168	Ile	Arg	Asp	Val	Gly	Gly	Arg	Arg	Pro	Lys	Cys	Gly	Pro	Cys
169			30			35					40			Pro
171	gag	ggc	tgc	ccg	g	c	c	tgc	ccg	g	gg	atc	tgc	255
172	Glu	Gly	Cys	Pro	Ala	Pro	Ala	Pro	Cys	Pro	Ala	Pro	Gly	Ile
173			45			50					55			Ser
175	ctc	gac	gag	tgc	ggc	tgc	tgc	gcc	cgc	tgc	gga	gcc	gag	303
176	Leu	Asp	Glu	Cys	Gly	Cys	Cys	Ala	Arg	Cys	Leu	Gly	Ala	Glu
177			60			65					70		75	Gly
179	agc	tgc	ggg	ggc	ccg	ggc	ggg	cgc	tgt	ggc	ccc	ggc	ctg	351
180	Ser	Cys	Gly	Gly	Arg	Ala	Gly	Gly	Arg	Cys	Gly	Pro	Gly	Leu
181						80					85		90	Val
183	g	cg	ag	c	g	cc	g	c	g	cc	g	gg	ctc	399
184	Ala	Ser	Gln	Ala	Ala	Gly	Ala	Ala	Pro	Glu	Gly	Thr	Gly	Leu
185						95					100		105	Cys
187	tgc	gc	c	g	c	g	cc	g	tgc	gg	tcc	gac	g	447
188	Cys	Ala	Gln	Arg	Gly	Thr	Val	Cys	Gly	Ser	Asp	Gly	Arg	Ser
189						110					115		120	Tyr
191	agc	gtc	tgc	ggc	cc	g	tc	tgc	cc	g	cc	g	cc	495
192	Ser	Val	Cys	Ala	Leu	Arg	Leu	Arg	Ala	Arg	His	Thr	Pro	Arg
193						125					130		135	Ala
195	ccc	gg	t	cac	a	ag	g	cg	cc	g	c	tgc	g	543
196	Pro	Gly	His	Leu	His	Lys	Ala	Arg	Asp	Gly	Pro	Cys	Glu	Phe
197						140					145		150	Ala
199	gt	gt	gt	gt	c	cc	c	gt	ca	ac	gt	cc	gg	591
200	Val	Val	Val	Val	Pro	Pro	Arg	Ser	Val	His	Asn	Val	Thr	Gly
201						160					165		170	Ala
203	gt	gg	ct	tg	t	tt	gaa	gt	gg	gt	cc	acc	cc	639
204	Val	Gly	Leu	Ser	Cys	Glu	Val	Arg	Ala	Val	Pro	Thr	Pro	Val
205						175					180		185	Ile
207	tgg	aga	a	ag	gt	c	cc	t	gg	gg	cc	aa	gca	687
208	Trp	Arg	Lys	Val	Thr	Lys	Ser	Pro	Glu	Gly	Thr	Gln	Ala	Glu
209						190					195		200	Glu
211	ctg	cct	gg	gac	cat	gt	aat	ata	gct	caa	gt	cg	gg	735
212	Leu	Pro	Gly	Asp	His	Val	Asn	Ile	Ala	Val	Gln	Val	Arg	Gly
213						205					210		215	Pro
215	tct	gac	cat	g	cc	tg	att	tt	atc	aa	cc	ct	cg	783
216	Ser	Asp	His	Glu	Ala	Thr	Ala	Trp	Ile	Leu	Ile	Asn	Pro	Lys
217						220					225		230	235
219	gag	gat	g	ag	gt	tac	c	tg	cat	gca	gg	aa	atg	831
220	Glu	Asp	Glu	Gly	Val	Tyr	Gln	Cys	His	Ala	Ala	Asn	Met	Glu
221						240					245		250	
223	g	c	tg	cc	ca	ac	gt	tt	ca	gt	at	gt	aaa	879

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224 Ala Glu Ser His Ser Thr Val Thr Val Leu Asp Leu Ser Lys Tyr Arg
225      255          260          265
227 agc ttc cac ttc cca gct ccc gat gac cgc atg tga tggagaaatg      925
228 Ser Phe His Phe Pro Ala Pro Asp Asp Arg Met
229      270          275
231 tacatgttct aagtcatttt cagtattttt caccatgtt atgagatatt tgagggtggct    985
233 tataagacctt gtaaaaaaaaaaaa aaaaaa      1009
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237 <211> LENGTH: 278
238 <212> TYPE: PRT
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241 <400> SEQUENCE: 6
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247 Pro Leu Leu Pro Pro Leu Ser Pro Ser Leu Gly Ile Arg Asp Val Gly
248      20           25          30
251 Gly Arg Arg Pro Lys Cys Gly Pro Cys Arg Pro Glu Gly Cys Pro Ala
252      35           40          45
255 Pro Ala Pro Cys Pro Ala Pro Gly Ile Ser Ala Leu Asp Glu Cys Gly
256      50           55          60
259 Cys Cys Ala Arg Cys Leu Gly Ala Glu Gly Ala Ser Cys Gly Gly Arg
260 65           70           75          80
263 Ala Gly Gly Arg Cys Gly Pro Gly Leu Val Cys Ala Ser Gln Ala Ala
264      85           90          95
267 Gly Ala Ala Pro Glu Gly Thr Gly Leu Cys Val Cys Ala Gln Arg Gly
268      100          105          110
271 Thr Val Cys Gly Ser Asp Gly Arg Ser Tyr Pro Ser Val Cys Ala Leu
272      115          120          125
275 Arg Leu Arg Ala Arg His Thr Pro Arg Ala His Pro Gly His Leu His
276      130          135          140
279 Lys Ala Arg Asp Gly Pro Cys Glu Phe Ala Pro Val Val Val Val Pro
280 145          150          155          160
283 Pro Arg Ser Val His Asn Val Thr Gly Ala Gln Val Gly Leu Ser Cys
284      165          170          175
287 Glu Val Arg Ala Val Pro Thr Pro Val Ile Thr Trp Arg Lys Val Thr
288      180          185          190
291 Lys Ser Pro Glu Gly Thr Gln Ala Leu Glu Glu Leu Pro Gly Asp His
292      195          200          205
295 Val Asn Ile Ala Val Gln Val Arg Gly Gly Pro Ser Asp His Glu Ala
296      210          215          220
299 Thr Ala Trp Ile Leu Ile Asn Pro Leu Arg Lys Glu Asp Glu Gly Val
300 225          230          235          240
303 Tyr Gln Cys His Ala Ala Asn Met Val Gly Glu Ala Glu Ser His Ser
304      245          250          255
307 Thr Val Thr Val Leu Asp Leu Ser Lys Tyr Arg Ser Phe His Phe Pro
308      260          265          270
311 Ala Pro Asp Asp Arg Met
312      275
315 <210> SEQ ID NO: 7

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 325 tgccggccagg aggctgccc ggccgtctcgat ccctgtccccgg cgccggggat 180
 327 gacgagtgcg gctgtgtcgcc cccgtgtcgat ggagccgagg ggcgcgatcg cggggggccgc 240
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 331 gagggcacccg ggctgtgtcgat gtgcgcgcac ccgtgtgtccg tctgcgggttc cgcacgggtcg 360
 333 tgcgtaccatca ggcgtgtcgcc gctgtgtcgat ccgtgtgtccg acacgcggcc 420
 335 ggtcacccatgc acaaggcgccg cgcacggccct tgccgtgtcgat ccctgtgttgc cgtgtttcc 480
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 345 taccatgtgcc atgcagccaa catgggtggat gaggctgttgc cccacagcac agtgcacgggtt 780
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 351 <211> LENGTH: 16
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 353 <213> ORGANISM: Homo sapiens
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 361 <210> SEQ ID NO: 9
 362 <211> LENGTH: 27
 363 <212> TYPE: PRT
 364 <213> ORGANISM: Homo sapiens
 366 <400> SEQUENCE: 9
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 372 Pro Leu Leu Pro Pro Leu Ser Pro Ser Leu Gly
 373 20 25
 376 <210> SEQ ID NO: 10
 377 <211> LENGTH: 251
 378 <212> TYPE: PRT
 379 <213> ORGANISM: Homo sapiens
 381 <400> SEQUENCE: 10
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 384 1 5 10 15
 387 Glu Gly Cys Pro Ala Pro Ala Pro Cys Pro Ala Pro Gly Ile Ser Ala
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 392 35 40 45
 395 Ser Cys Gly Gly Arg Ala Gly Gly Arg Cys Gly Pro Gly Leu Val Cys
 396 50 55 60
 399 Ala Ser Gln Ala Ala Gly Ala Ala Pro Glu Gly Thr Gly Leu Cys Val
 400 65 70 75 80

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